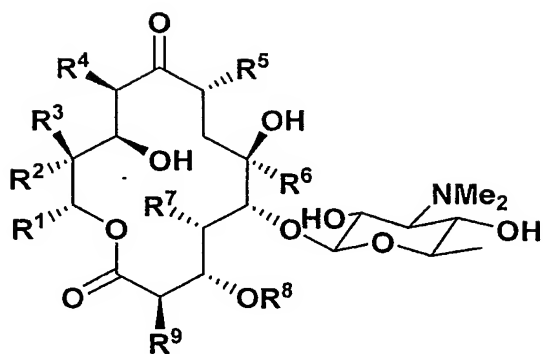
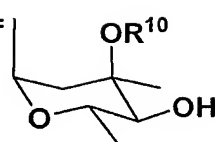


Figure 1A

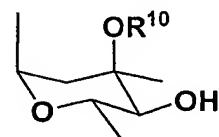
5-O-dedesosaminy-5-O-mycaminosyl-erythromycin B

$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 = -H$ $R^8 =$ $R^{10} = CH_3$



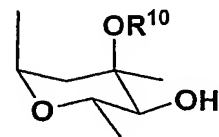
5-O-dedesosaminy-5-O-mycaminosyl-erythromycin A

$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 = -OH$ $R^8 =$ $R^{10} = CH_3$

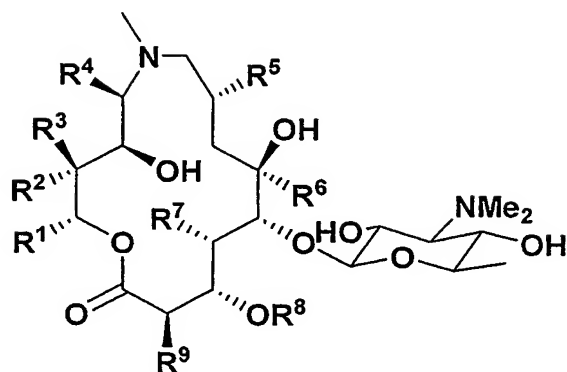


5-O-dedesosaminy-5-O-mycaminosyl-erythromycin C

$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 = -OH$ $R^8 =$ $R^{10} = H$



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Figure 1B

5-O-dedesosaminy-5-O-mycaminosyl-azithromycin

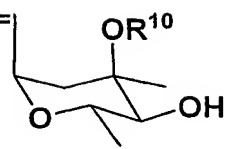
R¹ = C₂H₅ R² = R⁴ = R⁵ = R⁶ = R⁷ = R⁹ = -CH₃ R³ = -OH R⁸ =  R¹⁰ = CH₃

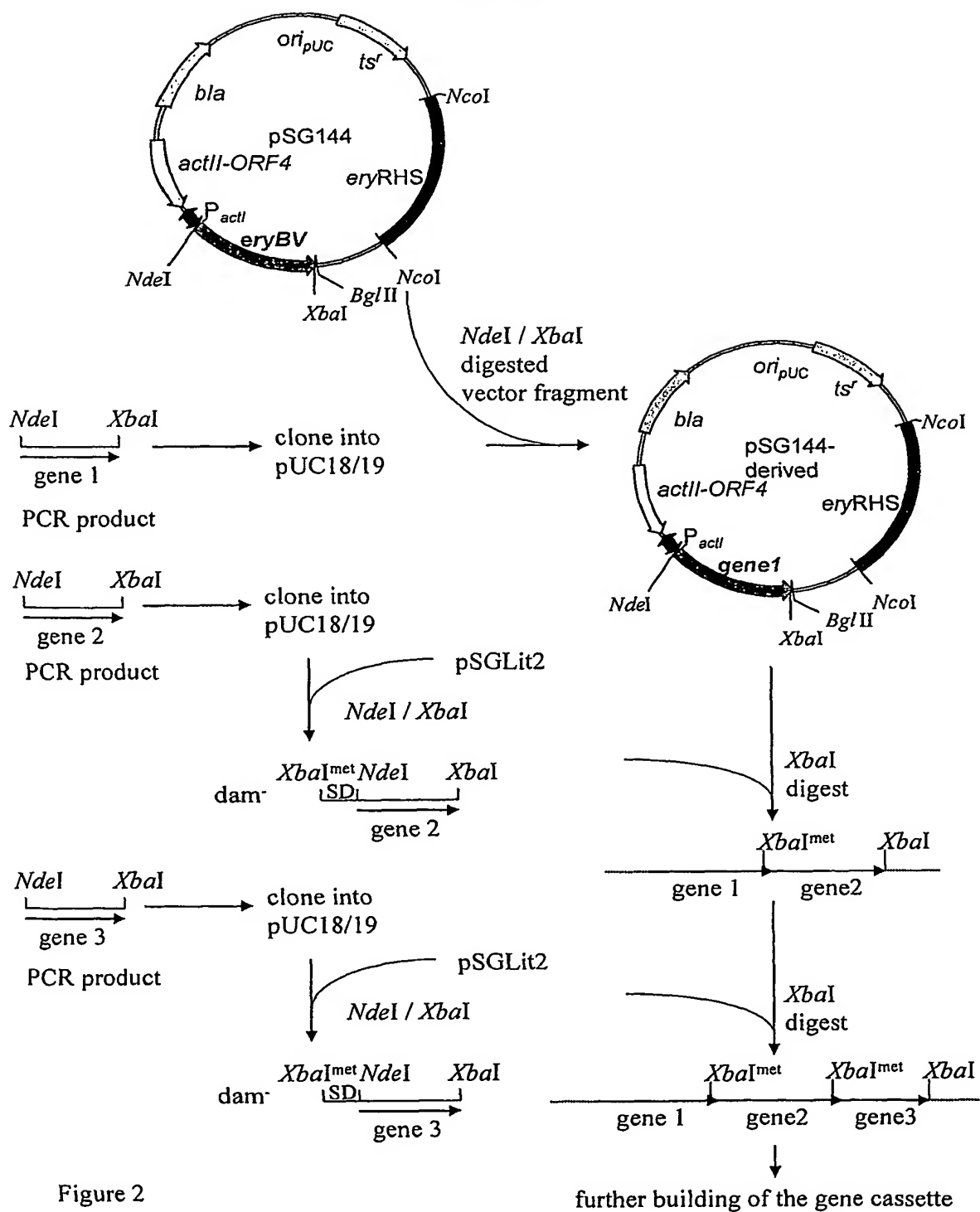
Figure 2

Figure 3

TylA1.pep x u08223.em_pro2

5

1 MNDRPRRAMKGIILAGGSGTRLRPLTGTLSKQLLPVYDKPMIYYPLSVLM 50
|||||

10 1 MNDRPRRAMKGIILAGGSGTRLRPLTGTLSKQLLPVYDKPMIYYPLSVLM 50
51 LAGIREIQIISSKDHLDLFRSLLGEGDRLGLSISYAEQREPRGIAEAFLI 100
|||||

15 51 LAGIREIQIISSKDHLDLFRSLLGEGDRLGLSISYAEQREPRGIAEAFLI 100
101 GARHIGGDAAALILGDNVFGPGFSSVLTGTVARLDGCELFGYPVKDAHR 150
|||||

20 101 GARHIGGDAAALILGDNVFGPGFSSVLTGTVARLDGCELFGYPVKDAHR 150
151 YGVGEIDSGGRLLSLEEKPRRPRSNLAVTGLYLYTNDVVEIARTISPSAR 200
|||||

25 151 YGVGEIDSGGRLLSLEEKPRRPLEP.GRHRLYLYTNDVVEIARTISPSAR 199
201 GELEITDVNKVYLEQGRARLTELGRGFAWLDMGTHDSLLQAGQYVQLLEQ 250
|||||

30 200 GELEITDVNKVYLEQGRA.AHGAGAVVAWLDMGTHDSLLQAGQYVQLLEQ 248
251 RQGERIACIEEIAMRMGFISAEQCYRLGQELRSSSYGSYIIDVAMRGAAA 300
|||||

35 249 RQGERIACIEEIAMRMGFISAEQCYRLGQELRSSSYGSYIIDVAMRGAAA 298
301 DSRAQ 305
|||||

299 DSRAQ 303

Figure 4

TylAII.pep x u08223.em_pro2

1 MRVLVTGGAGFIGSHFTGQLLT GAYPDLGATRTVVLDKLT YAGNPANLEH 50
|||||
1 MRVLVTGGAGFIGSHFTGQLLT GAYPDLGATRTVVLDKLT YAGNPANLEH 50

51 VAGHPDLEFVRGDIADQALVRRRLMEGVGLVVHFAAESHVDRSIESSEAFV 100
|||||
51 VAGHPDLEFVRGDIADHGWWRRRLMEGVGLVVHFAAESHVDRSIESSEAFV 100

101 RTNVEGTRVLLQAAVDAGVGRFVHISTDEVYGSIAEGSWPEDHPLAPNSP 150
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101 RTNVEGTRVLLQAAVDAGVGRFVHISTDEVYGSIAEGSWPEDHVPAPNSP 150

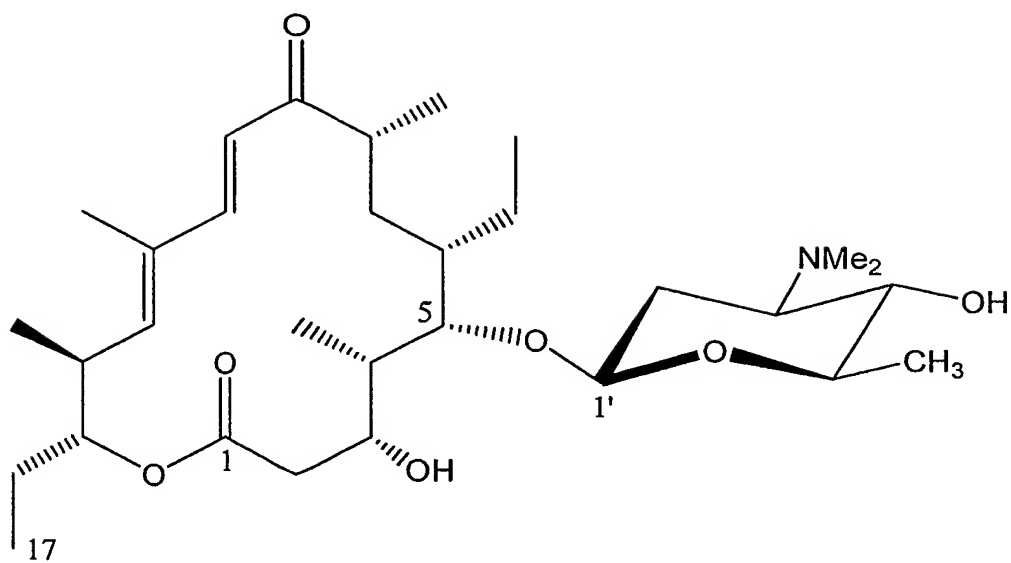
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|||||
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201 DGLPVPLYGDGGNTREWLHVDDHCRGVALVAAGGRPGVIYNIGGGTEL TN 250
|||||
201 DGLPVPLYGDGGNTREWLHVDDHCRGVALVGAGGRPGVIYNIGGGTEL TN 250

251 AELTDRILELCGADRSAYRRVAD RPHGDRRYSVDTTKIREELGYAPRTGI 300
|||||
251 AELTDRILELCGADRSALRRVAD RPHGDRRYSVDTTKIREELGYAPRTGI 300

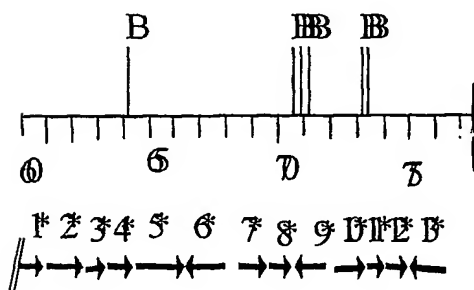
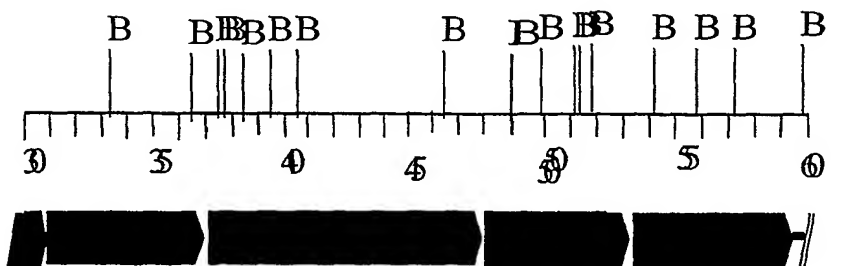
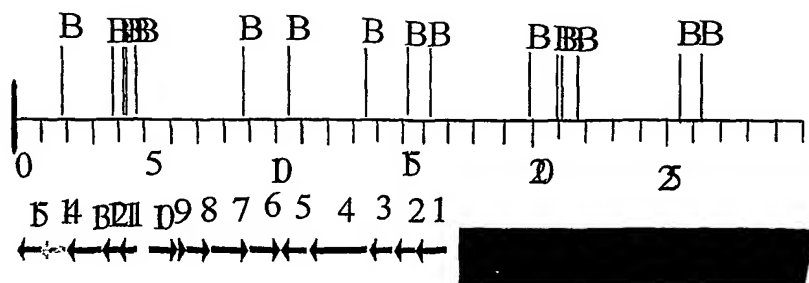
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|||||
301 TEGLAGTVAWYRDNRRAWWEPLKRSPGGRELER A 333

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Figure 5

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Figure 6



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Figure 7

5 1 GGCATGCCTT CGGGGTGTGC GCGGGCGCCT CAGAGCGTGG CCAGTACCTC
 51 GTGCAGGGCC GCGATCACCT TGTCTGTAC GTCGGGCGCG AGCCCCGGGT
10 101 ACATCGGCAG CGAGAAGATC TCGTCCGCCA GCCGCTCCGT CACCGGCAGC
 151 GAGCCCTTGG CGTACCCCAG GTGCGCGAAG CCCGTCATGG TGTGCACGGG
 201 CCACGGGTAA CTGATGTTGA GCGAGATCCC GTACGACTTG AGCGCCTCGA
15 251 TGATGTCGTC CCGGCGCGGG TGGCGGACGA CGTACACGTA ATACACGTGG
 301 TCGTTGCCCT CGGTGACGGA CGGCAGCACC AGGCCGCCGG GGCCCGTCAG
 351 GTTGCGGAGT CCTTCGGCGT AACGCGGGG GACCGCGCGC CGGCCCTCGA
20 401 TGTAGCGGTC GAGGCGGGTG AGCTTGCGGC GCAGGATCTC CGCCTGCACC
 451 TCGTCGAGCC GGCTGTTGTG GCCGGGCGTC TGCACGACGT AGTACACGTC
25 501 CTCCATGCCG TAGTAGCGCA GCCGGCGCAG CGCACGGTCG ACGTCCGCGT
 551 CGTCGGTCAG CACGGCCCCG CCGTCGCCGT ACGCACCGAG GACCTTCGTC
 601 GGGTAGAACG AGAAGGCGGC GGCCTCGCCC AGCGTGCCGG CCAGCTCGCC
30 651 GTGGTGGCGG GCACCGTGCG CCTGGGCGCA GTCCTCCAGC ACCACCAGGC
 701 CGTGCTGCTC GGCCAGGGCG CGCAAGGGCG CCATGTCGAC GCACTGCCCCG
35 751 TACAGGTGCA CCGGCAGCAG GGCCTTCGTG CGCGGGGTGA TGACGTCCGC
 801 GACCTGGTCG GTGTCCATGA GGTGGTCCTC GGC GCGGACG TCGACGAAGA
 851 CGGGCGTGGC ACCGGTGCCG TCGATGGCCA CCACCGTCGG CGCGGCCGTG
40 901 TTGGAGACGG TGACGACCTC GTCCCCCGGG CCCACCCCGA GCGCCTGCAG
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45 1001 GGCCGTGGTA GTCCGCGAAC TCCTTCTCGA ACCCGTCCAC GCTGGGGCCG
 1051 AGGACCAACT GCCCGGAGGC GAAGACGGTC TCGACGGCGT CGAGGAGGTC
 1101 CGCGCGTTTG TTCTGGTATT CCGCCAGGTA GTCCCAGACG TAGGTAGTCA
50 1151 CGGAGAGCTC AACCTCCAGA GTGTTTCGAT GGGGTGGTGG GAAGCCGGTG
 1201 CGCGCGGACC AGGTCGTGCC AGCAGTCGCG GACCGACTCC CGCAGCGAAC
55 1251 GGCGCGGTGC CCAGCCCAGC AGGGCGCGCG CCGCGCCGGT GTCGACCCGC
 1301 AGCCAGTCCT CCCGGTGCCC GGGAGCCCGG CCCGGAGCCG GGCGCTCCAC
 1351 CACCCGCGCC GGAATGCCGC TCGCTCGAT GAACAGGCCG ACCAGGTCGC
60 1401 GGACGGCGAC CGCCTCGCCC CGCCCGATGC CGACGGCGAC CGGGACGGCC

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5 1551 CCGTCCCGGC GGCCGCCAGC AGCCGCTCGG CGACCTGGCC CAGCAGACTG
1601 ATCCGCGGGG TGCCGGGGCC CGACACGTTG GACACCCGTA GCACCACACC
10 1651 GTCGACCCAC CCGCCCGAGG TGCCCGCAG CACCGCCTCG CTGGCGGCGA
1701 GCTTGCTCCT GCCGTACGCC GTGTCCGGGC GCGGTACGGC GTCGGCGCCC
1751 ACCGAACCGC CGGGCGTCAC CGGGCCGTAC TCCAGTACCG AGCCGAGGTG
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20 1901 ATGCTTCCGA CGGAGTTGAC GATCGTGTCC GGACGCTCCG CGTCCAGGGC
1951 GGCGGCCAGC GCCGCGGGAT CCGTACCGGC CAGGTCCAGG GTGACGCAGC
2001 GGTACGGCAT CGGCTCCTCG GGCGGGCGGC GGCCCACCAC CACCACGTCA
25 2051 CGGCCCCGCG CGGCGAACGC CGCGCACACA TGCCGGCCGA CGTACCCGGC
2101 GCCGCCCAGG ACCACGACGC TGCCACTGCC ACTGCCGCGC GGCATCGGAT
30 2151 CGTTCACCAT

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Figure 8

5 11301 CGTCAGTACA GCGTGTGGGC ACACGCCACC AGGGTGCGCA GCTCGATGTT
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 10 11451 ATCACGTAGC GGTTCGTGGC GTGGAAGAAG CGCCCGCCCT CCTCGGACTG
 11501 GACGGCGTCG TAGCGCACGT CCTGAGGCGG CGCGGACAGC ACGTCCTCCA
 15 11551 GGTACGGCGG GCCGGGCAGC CCCC GCGGAC CGGTGTGCTC CTGTGGCCGG
 11601 CACTGGACCG TGGGGGCCAG CTCGGCGACG TTCAGGTGCC CGACGTCCAC
 11651 CCGTGCCCGC ACGAGCGCGT GCAGCACGCC GTCGACGGAC TTGACCAGCA
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 25 11801 CCGCCCGCTC TCGTGGGCGA TCTCGTGCGG CGTGCGGTAC CAGCCGTCCG
 11851 CCGTCACCGT ATCGAGCGGC ACCCGGTTCT GCACCAGCTC CCGCAGGGCG
 11901 CGCACACCCG TGAACCACGT CAGGACCTCG GCCGTGCTGT GCCGCGCCGC
 30 11951 ACCCGGCGAG CCGAAGAAGG AGCGCAGCAC GGGGGACGGG GCGGACGCGT
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 40 12201 ATCGAGTCGA CCAGGACACG CGCCCGTCGC GGCCCCATGA ACAGGTCCAG
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 45 12301 CCTGCACGGT CGGCGACACC TGAAGAACGT TGACGTTCCC GGGCTCCATC
 12351 TTGGCCTGCA TCAGGAAGTG CAGCACCCCG TCGATCTCCC GCGCCACGAT
 12401 CCCGAGCAGC CCCACCTCCG GCTGCACGAT GATGGGCTGC GTCCAGCCCC
 50 12451 GCTCGGGCAG CCGGTCCGTA CGGACGTGCA GCCCCTCCAC GGAGAAGAAA
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 60 12701 ACCGGGCCCG ACCGCGTCCG CACGGCGCCG CGCGGCGCCG TCGGGGGCGG

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5 12751 GGGCGGATCG CGGCGGTACG GGTTCGCGGG CGGTGTCCGC GGCAGTGCGC
12801 GGCAGGACGG GGCAGGTGCT CGTGTCCGCG GCGGTACGCG GTGGGACGGT
12851 CCCGGTGGCC GTGTCCGCGG TGGCCGTGCC GGCAGGGGCG TCGCCGATGG
10 12901 TCCGGCACAC CTCGTCCATC CGGTCTTTCA GATAGAAGTG ACCGCCGGCG
12951 AAGGTGTGCA GGGCGAAGGG GCCCGTGGTC AGCTCCCGCC AGGCCCTCGC
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55 14051 TGTGGTAGAC CTCGCCCCGG CGCCCGCGGG TCGCCACCAG GCTGATCCCC
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60 14201 CGACCTTCTC GGGGTGCTGG TACGGGCCGT AGTTGTTGGA GCACCGGGTG

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5 14351 CCTCGCGCCA CGACCCCTCG GCGATCGAGC CGTACACCTC GTCCGTGGAG
14401 ACGTGGACGA ACCGGCCGGC CCCC GCCTCC ACCGCGGCCT GCAAGAGGAC
14451 TTGCGTCCCC CGTACGTTCG TCTCGACGAA CGCCGACGCG TCGGCGATGG
10 14501 AGCGGTCCAC GTGCGACTCC GCCGCGAAGT GGACCACGAC GTCCGCCCCC
14551 CGCACGACCC GGGACATCAC CTCCGCGTCC CGGATGTCGG CGTGCACGAA
15 14601 CTCCAGCGAC GGATGGTCCG CGACCGGGTC CAGGTTGGCG AGGTTCCCGG
14651 CATAGGTCAG CTTGTGACACC ACCACCGTCC GCGCCCCGGC CAGGTCCGGA
14701 TACGCCCCCG CCAGCAGTTG TCTGACGAAG TGCGAGCCGA TGAAGCCCCG
20 14751 ACCTCCGGTG ACCAGCAGCC GCATGGGAGC ACAGACCTTT CTTCCAGGGA
14801 CGGGAAACGG GGAGGCGGAC GGGGACGGAG GCGAGGGCGG TGGCTATGCG
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14951 TGTACCCCAT CCGCAGGGCG ATCTCCTCGA CGCAGGAGAT CCGCACGCCC
30 15001 TGCCGCTGCT CCAGGAGCTG GACGTACTGC CCCGCTTGCA GCAGCGAGCT
15051 GTGCGTGCCC ATGTCCAGCC AGGCGAACCC GCGCCCCAGT TCCGTCATAC
35 15101 GGGCGCGGCC CTGCTCCAGG TACACCTTGT TGACGTCGGT GATCTCCAGC
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60 15751 GTCTTCGTCA T

Figure 9

5 59800 G

59801 TGAGCCCCGC ACCCGCCACC GAGGACCCGG CCGCCGCCGG GCGCCGCCTG

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10 59901 CGCGCTCGTC CTGCGCGCCG AGGCCACCGA CCCGGCCCCG TACGAGGAGC

59951 GGATCCGGGC CCACGGGCCG CTCTTCCGCA GCGACCTGCT CGACACCTGG

15 60001 GTCACGGCGA GCAGGGCCGT CGCCGACGAA GTGATCACCT CACCCGCCTT

60051 CGACGGGCTC ACGGCCGACG GCGGGCGCCC CGGCGCGCGG GAACTGCCGC

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60151 GCCCTCACCG CCTGGGGCGG GCCGCTGCTG CCGGCGCCGC ACGAGCGGGC

60201 GCTGCGCGAG TCCGCCGAAC GCGGGGCCCA CACACTCCTC GACGGGGCGG

25 60251 AGGCCGCCCT GGCCGCCGAC GGCACCGTCG ACCTCGTCGA CGCGTACGCC

60301 CGCAGGCTCC CCGCGCTGGT CCTCCGCGAA CAGCTCGGCG TGCCGGAGGA

60351 GGCGGCGACC GCCTTCGAGG ACGCGCTGGC CGGCTGCCGC CGCACCTTGG

30 60401 ACGGCGCCCT GTGCCCGCAA CTCCTCCCGG ACGCCGTGGC GGGGGTGCGC

60451 GCGGAAGCCG CGCTGACCGC CGTGCTGGCC TCCGCCCTGC GCGGGACTCC

35 60501 GGCCGGCCGG GCCCCGACG CCGTCGCCGC CGCCCGCACC CTGGCCGTCG

60551 CGGCCGCCGA GCCCGCAGCC ACCCTCGTCG GCAACGCCGT ACAGGAGCTG

60601 CTGGCGCGTC CCGCGCAGTG GGCGGAGCTC GTACGCGACC CGCGCCTCGC

40 60651 GGCCGCCGCG GTGACCGAAA CGCTGCGTGT CGCCCCGCCC GTCCGCCTGG

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45 60751 GCCGGGGGGA GCGTCGTGAT CCTCGTCGCC GCCGTCAACC GCGCGCCCGT

60801 ATCCGCGGGA AGCGACGCCT CCACCACCGT CCCGCACGCC GCGGGCCGGC

60851 CCCGTACCTC CGCCCCCTCC GTCCCCTCAG CCCCTTCGA CCTCACACGG

50 60901 CCCGTGGCCG CGCCCGGGCC GTTCGGGCTC CCCGGCGACC TGCATTCCG

60951 CCTCGGCGGG CCCCTGGTCG GAACGGTCGC CGAAGCCGCG CTCGGTGCGC

55 61001 TGGCCGCACG GCTCCCCGGT CTGCGCGCCG CCGGGCCGGC CGTGCGGCGC

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60 61151 GTGCCCCGAT GCGTATCCTG CTGACGTCGT TCGCGCACAA CACGCACTAC

5 61201 TACAACCTGG TCCCCCTCGG CTGGGCGCTG CGCGCCGCCG GGCACGACGT
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61301 TGACCGCCGT CCCCCTGGGC GACGACACGG CCATCGTCGA GCTGATCACC
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10 61401 CACCCGCGAC GAGCCGCTGT CCTGGGAACA CGCCCTCGGA CAGCAGACGA
61451 TCATGTCGGC CATGTGCTTC TCGCCGCTGA ACGGCGACAG CACCATCGAC
15 61501 GACATGGTGG CGCTGGCCCG TTCCTGGAAG CCGGACCTCG TCCTGTGGGA
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25 61751 CGGACACGAT CGAGGAACTG TTCGCCGGGC AGTGGACGAT CGACCCCAGC
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61851 CGTGCCGTAC AACGGCGCCT CGGTGCTCCC CGCCTGGCTC TCCGAGCCGC
30 61901 CTGCCCAGCC CCGGGTCTGC GTCACCCTCG GCGTCTCCAC CCGGAGACCC
61951 TACGGCACGG ACGGCGTCCC GTTCCACGAA CTGCTGGCCG GACTGGCCGA
35 62001 CGTGGACGCC GAGATCGTCG CCACCCTCGA CGCGGGGCAG CTCCCGACG
62051 CCGCCGGTCT GCCCGGCAAT GTGCGCGTCG TCGACTTCGT GCCGCTGGAC
62101 GCCCTGCTGC CGAGCTGCGC CGCGATCGTC CACCACGGAG GCGCGGGAAC
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45 62251 ATCGCCCTGG ACCCCGGGGA ACTGGGCGTG GACACCCTGC GCGGCGCCGT
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50 62401 GAACGCCTCA CCGCCGCGCA CCGCCGCGCC TGATCCCGCC AAGGAGCCCC
62451 CATGAACCTC GAATACAGCG GCGACATCGC CCGGTTGTAC GACCTGGTCC
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62601 CGGAACGGGG ATGCACCTGC GGCACCTCGG CGACCTCTTC GAGGAGGTGG
60 62651 CCGGGGTGGA GATGTCCCCC GACATGCTGG CCATCGCGCA GCGGCGCAAC

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5 62801 ACCAGCGGGA ACTGGACGCG GCGATCGGCC GGTTCGCCGC GCACCTGCCG
62851 TCCGGCGGGG TCGTGATCGT CGATCCCTGG TGGTTCCCGG AGACGTTTAC
10 62901 ACCGGGGTAC GTCGGCGCGA GCCTCGTCTG GCGCGAGGGC CGCACCATCG
62951 CGCGCTTCTC CCACTCCGCG CTCGAGGACG GCGCGACCCG GATCGATGTG
63001 GACTACCTCG TCGGCGTGCC GGGGGAGGGG GTGCGGCACT TGAAGGAGAC
15 63051 CCATCGGATC ACGCTTTTCG GGCCTGCGCA GTACGAGGCG GCCTTCACCG
63101 CGGCGGGGAT GTCCGTCGAG TACCTCCCGC ACGCCGCCAC CGACCGCGGA
20 63151 CTCTTCGTCG GCGTCCAGGC CTGA

25

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Figure 10

1 MKGIILAGGS GTRLRPLTGA LSKQLLPVYD KPMIYYPLSV LMLAGIRDIQ
51 IITSKTHLEM FRLLGDGSR IGISVGYAEQ EEPRGIAEAF LIGEEHIGDD
101 PVALILGDNV FHGPGFSSVL ASTAARLDGC ELFGYPVKDP RRYGVGEVDA
151 EGRLVSLEEK PEKPRSHLAV TGLYFYDNGV VDIARRLTPS PRGELEITDV
201 NKVYLEQGRA RMTELGRGFA WLDMGTHSSL LQAGQYVQLL EQRQGVRI SC
251 VEEIALRMGY ISARQCHEL G RELESSSYGR YLMDVAETLM SGPAA

Figure 11

1 MRLLVTTGGAG FIGSHFVRQL LAGAYPDLAG ARTVVVDKLT YAGNLANLDP
51 VADHPSLEFV HADIRDAEVM SRVVRGADV VHFAAESHVD RSIADASAFV
101 ETNVRGTQVL LQAAVEAGAG RFVHVSTDEV YGSIAEGSWR EEQPLAPNSP
151 YAASKAASDL LALAYHRTYG LPVVVTRCSN NYGPYQHPEK VVPLFATNLL
201 DGLTVPLYSD GGNSRDWLHV DDHCRGISLV ATRGRPGEVY HIGGGTELTN
251 RELTKRLLGL CGADASSVRH VADRPBGHDLR YALDIGKITG ELGYAPRTDF
301 TTGLADTVRW YAENRAWWEP LKKAQAEARR TD

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Figure 12

1 VSTPSAPPVP GAPSPAGHPD EGLWVRRYRP VRDPELRLVC FPHAGGAATS
51 FAALARGLDE TVEALAVQYP GRQDRRHEPF IPSISGLVDQ VVPEILRWAD
101 RPLALFGHSM GATVAFEVAR RLRGSGQASP VHLLVSGRRA PTVRRRDVAH
151 LLDDDALIAE IATLQGTEDA VLQDEELLRL ALPAIRNDYR AAGTYAYVPG
201 GALDCPVTVL TGDRDPDVPL EEARAWRELT TGPFALHTFA GGHFYLNDRM
251 DEVCRTIGDA LAGTATADTA TGTVPPTAA DTSTGVPVPR TAADTAREPV
301 PPRSAPAPHG AARRRADAVR PGDPVDTARR VLVSARTADS AVTPFDGISG
351 WLAERLRAGR FDVSRVPFAE LRGWSFHPGT GNLHHASGRF FSVEGLHVRT
401 DRLPERGWTQ PIIVQPEVGL LGIVAREIDG VLHFLMQAKM EPGNVNVLQV
451 SPTVQATRSN FTGVHRGRDI RYLDLFMGPR RARVLVDSIQ SEQADWFLAK
501 RNRNMIVELA ADDDLDIGED FRWLTGQLR RLLMLDNVVN MDARSILACL
551 PTADADASAP SPVLRSEFGS PGAARHTTAE VLTWFTGVRA LRELVQNRVP
601 LDTVTDAGWY RTPHEIAHES GRHFRVMAAE VSASSREVTS WTQPLIEPRL
651 PGLMALLVKS VDGVLHALVR ARVDVGHLNV AELAPTQCR PQEHTGPRGL
701 PGPPYLEDVL SAPPQDVRYD AVQSEEGGRF FHAQNRYVIV EVPHDFPEDA
751 PDDFAWLSLG QLTGLLAHGN YLNIELRTL V ACAHTLY

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Figure 13

5 1 MVNDPMPRGS GSGSVVVLGG AGYVGRHVCA AFAARGRDVV VVGRRPPEEP
51 MPYRCVTLDL AGTDPAALAA ALDAERPDTI VNSVGSIWGR TDEQMWSATA
101 VPTLRLLEAL ALMSARPLV HLGSVLEYGP VTPGGSVGAD AVPRPDTAYG
0 151 RSKLAASEAV LRGTSGGWVD GVVLRVSNVS GPGTPRISLL GQVAERLLAA
201 AGTGAEAVVE LSRLRAHRDY VDVRDVADAV VAAARAPAVP VAVGIGRGEA
5 251 VAVRDLVGLF IEASGIPARV VERPAPGRAP GHREDWLRVD TGAARALLGW
301 APRRSLRESV RDCWHDLVRA HRLPTTPSKH SGG

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Figure 14

5 1 VTTYVWDYLA EYQNERADLL DAVETVFASG QLVLGPSVDG FEKEFADYHG
 51 LRHCGGVDNG TNAVKLGLQA LGVGPGDEVV TVSNTAAPT V AIDGTGATP
10 101 VFVDVRAEDH LMDTDQVADV ITPRTKALLP VHLYGQCVD APLRALAEQH
 151 GLVVLEDCAQ AHGARHHGEL AGTLGDAAAF SFYPTKVLGA YGDGGAVLTD
 201 DADVDRALRR LRYYG MEDVY YVVQTPGHNS RLDEVQAEIL RRKLTRLDRY
15 251 IEGRRAVARR YAEGLANLTG PGGLVLPSVT EGNDHVYYVY VVRHPRRDDI
 301 IEALKSYGIS LNISYPWPVH TMTGFAHLGY AKGSLPVT L ADEIFSLPM
 351 YPGLAPDVQD KVIAALHEVL ATL
20

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Figure 15

5 1 VSPAPATEDP AAAGRRRLQLT RAAQWFAGTQ DDPYALVLRA EATDPAPYEE
 51 RIRAHGFLFR SDLLDTWVTA SRAVADEVIT SPAFDGLTAD GRRPGARELP
10 101 LSGTALDADR ATCARFGALT AWGGPLLAP HERALRESAE RRAHTLLDGA
 151 EAALAADGTV DLVDAYARRL PALVLRQLG VPAAATAFE DALAGCRRTL
 201 DGALCPQLLP DAVAGVRAEA ALTAVLASAL RGTAPAGRAPD AVAAARTLAV
15 251 AAAEPAATLV GNAVQELLAR PAQWAEVLRD PRLAAAVTE TLRVAPPVRL
 301 ERRVARETD IAGQRLPAGG SVVILVAVN RAPVSAGSDA STTVPHAGGR
 351 PRTSAPSVPS APFDLTRPVA APGPFGPLPD LHFRLGGPLV GTVAEAAALGA
20 401 LAARLPGLRA AGPAVRRRRS PVLHGHRLP VAVARTARDL PATAPRN

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Figure 16

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1 MRILLTSFAH NTHYYNLVPL GWALRAAGHD VRVASQPSLT GTITGSGSLTA
51 VPVGDDTAIV ELITEIGDDL VLYQQGMDFV DTRDEPLSWE HALGQQTIMS
101 AMCFSPNLGD STIDDMVALA RSWKPDLVLW EPFTYAGPVA AHACGAAHAR
151 LLWGPDVVLN ARRQFTRLA ERPVEQREDP VGEWLTWTLE RHGLAADADT
201 IEELFAGQWT IDPSAGSLRL PVDGEVVPMPR FVPYNGASVV PAWLSEPPAR
251 PRVCVTLGVS TRETYGTDGV PFHELLAGLA DVDAEIVATL DAGQLPDAAG
301 LPGNVRVVDV VPLDALLPSC AAIVHHGGAG TCFTATVHGV PQIVVASLWD
351 APLKAHQLAE AGAGIALDPG ELGVDTLRGA VVRVLESREM AVAARRLADE
401 MLAAPTPAAL VPRLERLTAA HRRA

Figure 17

5 1 MNLEYSGDIA RLYDLVHQGK GKDYRAEAE LAALVTQRRP GARSLLDVAC
 51 GTGMHLRHLG DLFEEVAGVE MSPDMLAIAQ RRNPEAGIHR GDMRDFALGR
10 101 RFDVICMFS SIGHMRDQRE LDAAIGRFAA HLPSSGGVVIV DPWWFPETFT
 151 PGYVGASLVE AEGRTIARFS HSALEDGATR IDVDYLVGVP GEGVRHLKET
 201 HRITLFGRAQ YEAAFTAAGM SVEYLPHAAT DRGLEFVGVA
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